

Claims: -

1. A method for characterising nucleic acid molecules, which comprises the steps of:
 - 5 i) introducing a modified base which is a substrate for a DNA endonuclease into a target DNA molecule; and
 - ii) reacting the nucleic acid containing the modified base with said DNA endonuclease such that the nucleic acid is cleaved to generate an upstream fragment containing said modified base and bearing a 3' hydroxyl group.
- 10 2. A method according to Claim 1, wherein the modified base is introduced by enzymatic amplification of the nucleic acid.
3. A method according to Claim 1 or 2, wherein a nucleotide containing the modified base partially replaces a normal precursor nucleotide.
- 15 4. A method according to Claim 1 or 2, wherein a nucleotide containing the modified base totally replaces a normal precursor nucleotide.
5. A method according to Claim 1, wherein the modified base is introduced by chemical modification of an existing base.
- 20 6. A method according to any preceding claim, wherein the modified base is selected from inosine and uracil.

7. A method according to any preceding claim, wherein the endonuclease is a thermostable endonuclease.
8. A method according to any preceding claim, wherein the endonuclease cleavage reaction is carried out concurrently with a thermocycled amplification reaction using a thermostable endonuclease.
9. A method according to any one of Claims 2-8, wherein at least one of the primers for the amplification step is positioned adjacent a locus where a DNA sequence variation occurs.
10. A method according to any one of Claims 1-6 and 9, wherein the endonuclease is Endonuclease V from *E. coli*.
11. A method according to any preceding claim, wherein the upstream fragment generated in step ii) is used as a primer for a subsequent extension reaction.
12. A method according to Claim 11, wherein the extension is carried out using a DNA polymerase.
13. A method according to Claim 11, wherein the extension is carried out using a DNA ligase.
14. A method according to Claim 1, substantially as herein before described and exemplified
15. A method according to any preceding claim for use in detecting polymorphisms and mutations.

16. A method according to any one of Claims 1-14, for use in nucleic acid identification and profiling.

17. A method according to any one of Claims 1-14, for rapidly genotyping known polymorphisms and mutations.

5 18. A method according to any one of Claims 1-14, for scanning a nucleic acid sequence for the presence of known or unknown mutations and polymorphisms.